SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT:  BILLING-MEDEL, PATRICIA A.
                COHEN, MAURICE
                COLPITTS, TRACEY L.
                FRIEDMAN, PAULA N.
                HAYDEN, MARK
                KLASS, MICHAEL R.
                ROBERTS-RAPP, LISA
                RUSSELL, JOHN C.
                STROUPE, STEPHEN D.

(ii) TITLE OF THE INVENTION: REAGENTS AND METHODS FOR THE
        USEFUL FOR DETECTING DISEASES OF THE GASTROINTESTINAL
        TRACT

(iii) NUMBER OF SEQUENCES: 51

(iv) CORRESPONDENCE ADDRESS:
  (A) ADDRESSEE: Abbott Laboratories
  (B) STREET: 100 Abbott Park Road
  (C) CITY: Abbott Park
  (D) STATE: IL
  (E) COUNTRY: USA
  (F) ZIP: 60064-3500

(v) COMPUTER READABLE FORM:
  (A) MEDIUM TYPE: Diskette
  (B) COMPUTER: IBM Compatible
  (C) OPERATING SYSTEM: DOS
  (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
  (A) APPLICATION NUMBER:
  (B) FILING DATE:
  (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
  (A) APPLICATION NUMBER: 08/828,856
  (B) FILING DATE: 31-MAR-1997

(viii) ATTORNEY/AGENT INFORMATION:
  (A) NAME: Becker, Cheryl L.
  (B) REGISTRATION NUMBER: 35,441
  (C) REFERENCE/DOCKET NUMBER: 6068.US.P1

(ix) TELECOMMUNICATION INFORMATION:
  (A) TELEPHONE: 847/935-1729
  (B) TELEFAX: 847/938-2623
  (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 241 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
GCCAGGAATA ACTAGAGAGG AACAATGGGG TTATTCAGAG GTTTTGTTTT CCTCTTAGTT    60
CTGTGCCTGC TGCACCAGTC AAATACTTCC TTCATTAAGC TGAATAATAA TGGCTTTGAA   120
GATATTGTCA TTGTTATAGA TCCTAGTGTG CCAGAAGATG AAAAAATAAT TGAACAAATA   180
GAGGATATGG TGACTACAGC TTCTACGTAC CTGTTTGAAG CCACAGAAAA AAGATTTTTT   240
T                                                                  241
```

    (2) INFORMATION FOR SEQ ID NO:2:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 219 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
CTAGAGAGGA ACAATGGGGT TATTCAGAGG TTTTGTTTTC CTCTTAGTTC TGTGCCTGCT    60
GCACCAGTCA AATACTTCCT TCATTAAGCT GAATAATAAT GGCTTTGAAG ATATTGTCAT   120
TGTTATAGAT CCTAGTGTGC CAGAAGATGA AAAAATAATT GAACAAATAG AGGATATGGT   180
GACTACAGCT TCTACGTACC TGTTTGAAGC CACAGAAAA                          219
```

    (2) INFORMATION FOR SEQ ID NO:3:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 231 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (ix) FEATURE:
    (A) NAME/KEY: base_polymorphism
    (B) LOCATION: 3
    (D) OTHER INFORMATION: /note= "'N' represents an A or G or
        T or C polymorphism at this position"

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
TTNTGTAACG AAAAAACCCA TAATCAAGAA GCTCCAAGCC TACAAAACAT AAAGTGCAAT    60
TTTAGAAGTA CATGGGAGGT GATTAGCAAT TCTGAGGATT TTAAAAACAC CATACCCATG   120
GTGACACCAC CTCCTCCACC TGTCTTCTCA TTGCTGAAGA TCAGTCAAAG AATTGTGTGC   180
TTAGTTCTTG ATAAGTCTGG AAGCATGGGG GGTAAGGACC GCCTAAATCG A            231
```

    (2) INFORMATION FOR SEQ ID NO:4:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 237 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
TGGGGGGTAA GGACCGCCTA AATCGAATGA ATCAAGCAGC AAAACATTTC CTGCTGCAGA    60
CTGTTGAAAA TGGATCCTGG GTGGGGATGG TTCACTTTGA TAGTACTGCC ACTATTGTAA   120
ATAAGCTAAT CCAAATAAAA AGCAGTGATG AAAGAAACAC ACTCATGGCA GGATTACCTA   180
CATATCCTCT GGGAGGAACT TCCATCTGCT CTGGAATTAA ATATGCATTT CAGGTGA      237
```

          (2) INFORMATION FOR SEQ ID NO:5:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 216 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear


     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
CTTCCATCTG CTCTGGAATT AAATATGCAT TTCAGGTGAT TGGAGAGCTA CATTCCCAAC    60
TCGATGGATC CGAAGTACTG CTGCTGACTG ATGGGGAGGA TAACACTGCA AGTTCTTGTA   120
TTGATGAAGT GAAACAAAGT GGGGCCATTG TTCATTTTAT TGCTTTGGGA AGAGCTGCTG   180
ATGAAGCAGT AATAGAGATG AGCAAGATAA CAGGAG                             216
```

          (2) INFORMATION FOR SEQ ID NO:6:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 201 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

     (ix) FEATURE:
        (A) NAME/KEY: base_polymorphism
        (B) LOCATION: 24
        (D) OTHER INFORMATION: /note= "'N' represents an A or G or
             T or C polymorphism at this position"

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
AATTGATAGT ACAGTGGGAA AGGNCACGTT CTTTCTCATC ACATGGAACA GTCTGCCTCC    60
CAGTATTTCT CTCTGGGATC CCAGTGGAAC AATAATGGAA AATTTCACAG TGGATGCAAC   120
TTCCAAAATG GCCTATCTCA GTATTCCAGG AACTGCAAAG GTGGGCACTT GGGCATACAA   180
TCTTCAAGCC AAAGCGAACC C                                             201
```

          (2) INFORMATION FOR SEQ ID NO:7:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 241 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear


     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
GCAAATTCTT CTGTGCCTCC AATCACAGTG AATGCTAAAA TGAATAAGGA CGTAAACAGT    60
TTCCCCAGCC CAATGATTGT TTACGCAGAA ATTCTACAAG GATATGTACC TGTTCTTGGA   120
GCCAATGTGA CTGCTTTCAT TGAATCACAG AATGGACATA CAGAAGTTTT GGAACTTTTG   180
GATAATGGTG CAGGCGCTGA TTCTTTCAAG AATGATGGAG TCTACTCCAG GTATTTTACA   240
G                                                                  241
```

          (2) INFORMATION FOR SEQ ID NO:8:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 242 base pairs
        (B) TYPE: nucleic acid

```
        (C)  STRANDEDNESS: single
        (D)  TOPOLOGY: linear



    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTGCAGGCGC TGATTCTTTC AAGAATGATG GAGTCTACTC CAGGTATTTT ACAGCATATA      60
CAGAAAATGG CAGATATAGC TTAAAAGTTC GGGCTCATGG AGGAGCAAAC ACTGCCAGGC     120
TAAAATTACG GCCTCCACTG AATAGAGCCG CGTACATACC AGGCTGGGTA GTGAACGGGG     180
AAATTGAAGC AAACCCGCCA AGACCTGAAA TTGATGAGGA TACTCAGACC ACCTTGGAGG     240
AT                                                                   242
```

            (2)  INFORMATION FOR SEQ ID NO:9:

        (i)  SEQUENCE CHARACTERISTICS:
            (A)  LENGTH: 233 base pairs
            (B)  TYPE: nucleic acid
            (C)  STRANDEDNESS: single
            (D)  TOPOLOGY: linear


    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
CCCGCCAAGA CCTGAAATTG ATGAGGATAC TCAGACCACC TTGGAGGATT TCAGCCGAAC      60
AGCATCCGGA GGTGCATTTG TGGTATCACA AGTCCCAAGC CTTCCCTTGC CTGACCAATA     120
CCCACCAAGT CAAATCACAG ACCTTGATGC CACAGTTCAT GAGGATAAGA TTATTCTTAC     180
ATGGACAGCA CCAGGAGATA ATTTTGATGT TGGAAAAGTT CAACGTTATA TCA           233
```

            (2)  INFORMATION FOR SEQ ID NO:10:

        (i)  SEQUENCE CHARACTERISTICS:
            (A)  LENGTH: 313 base pairs
            (B)  TYPE: nucleic acid
            (C)  STRANDEDNESS: single
            (D)  TOPOLOGY: linear

        (ix)  FEATURE:
            (A)  NAME/KEY: base_polymorphism
            (B)  LOCATION: 22
            (D)  OTHER INFORMATION: /note= "'N' represents an A or G or
                  T or C polymorphism at this position"

        (ix)  FEATURE:
            (A)  NAME/KEY: base_polymorphism
            (B)  LOCATION: 44
            (D)  OTHER INFORMATION: /note= "'N' represents an A or G or
                  T or C polymorphism at this position"

    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
CCAATACCCA CCAAGTCAAA TNACAGACCT TGATGCCACA GTTNATGAGG ATAAGATTAT      60
TCTTACATGG ACAGCACCAG GAGATAATTT TGATGTTGGA AAAGTTCAAC GTTATATCAT     120
AAGAATAAGT GCAAGTATTC TTGATCTAAG AGACAGTTTT GATGATGCTC TTCAAGTAAA     180
TACTACTGAT CTGTCACCAA AGGAGGCCAA CTCCAAGGAA AGCTTTGCAT TTAAACCAGA     240
AAATATCTCA GAAGAAAATG CAACCCACAT ATTTATTGCC ATTAAAAGTA TAGATAAAGC     300
ATTTGGCATC AAA                                                       313
```

            (2)  INFORMATION FOR SEQ ID NO:11:

        (i)  SEQUENCE CHARACTERISTICS:
            (A)  LENGTH: 242 base pairs
            (B)  TYPE: nucleic acid
            (C)  STRANDEDNESS: single
            (D)  TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
AAGTATTCTT GATCTAAGAG ACAGTTTTGA TGATGCTCTT CAAGTAAATA CTACTGATCT        60
GTCACCAAAG GAGGCCAACT CCAAGGAAAG CTTTGCATTT AAACCAGAAA ATATCTCAGA       120
AGAAAATGCA ACCCACATAT TTATTGCCAT TAAAAGTATA GATAAAAGCA ATTTGACATC       180
AAAAGTATCC AACATTGCAC AAGTAACTTT GTTTATCCCT CAAGCAAATC CTGATGACAT       240
TG                                                                     242
```

        (2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 208 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

     (ix)   FEATURE:
       (A) NAME/KEY: base_polymorphism
       (B) LOCATION: 2
       (D) OTHER INFORMATION: /note= "'N' represents an A or G or
            T or C polymorphism at this position"

     (ix)   FEATURE:
       (A) NAME/KEY: base_polymorphism
       (B) LOCATION: 4
       (D) OTHER INFORMATION: /note= "'N' represents an A or G or
            T or C polymorphism at this position"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
ANANAATGCA ACCCACATAT TTATTGCCAT TAAAAGTATA GATAAAAGCA ATTTGACATC        60
AAAAGTATCC AACATTGCAC AAGTAACTTT GTTTATCCCT CAAGCAAATC CTGATGACAT       120
TGATCCTACT CCTACTCCTA CTCCTACTCC TGATAAAAGT CATAATTCTG GAGTTAATAT       180
TTCTACGCTG GTATTGTCTG TGATTGGG                                          208
```

        (2) INFORMATION FOR SEQ ID NO:13:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 201 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
CTCCTACTCC TACTCCTGAT AAAAGTCATA ATTCTGGAGT TAATATTTCT ACGCTGGTAT        60
TGTCTGTGAT TGGGTCTGTT GTAATTGTTA ACTTTATTTT AAGTACCACC ATTTGAACCT       120
TAACGAAGAA AAAAATCTTC AAGTAGACCT AGAAGAGAGT TTTAAAAAAC AAAACAATGT       180
AAGTAAAGGA TATTTCTGAA T                                                 201
```

        (2) INFORMATION FOR SEQ ID NO:14:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 301 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
   ·   (D) TOPOLOGY: linear

     (ix)   FEATURE:
       (A) NAME/KEY: base_polymorphism
       (B) LOCATION: 111
       (D) OTHER INFORMATION: /note= "'N' represents an A or G or
            T or C polymorphism at this position"

```
(ix)  FEATURE:
      (A)  NAME/KEY: base_polymorphism
      (B)  LOCATION: 244
      (D)  OTHER INFORMATION: /note= "'N' represents an A or G or
           T or C polymorphism at this position"

(ix)  FEATURE:
      (A)  NAME/KEY: base_polymorphism
      (B)  LOCATION: 284
      (D)  OTHER INFORMATION: /note= "'N' represents an A or G or
           T or C polymorphism at this position"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
TCTGTTGTAA TTGTTAACTT TATTTTAAGT ACCACCATTT GAACCTTAAC GAAGAAAAAA    60
ATCTTCAAGT AGACCTAGAA GAGAGTTTTA AAAAACAAAA CAATGTAAGT NAAGGATATT   120
TCTGAATCTT AAAATTCATC CCATGTGTGA TCATAAACTC ATAAAAATAA TTTTAAGATG   180
TCGGAAAAGG ATACTTTGAT TAAATAAAAA CACTCATGGA TATGTAAAAA CTGTCAAGAT   240
TAANATTTAA TAGTTTCATT TATTTGTTAT TTTATTTGTA AGANATAGTG ATGAACAAAG   300
A                                                                   301
```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 229 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
GAAAAAAATC TTCAAGTAGA CCTAGAAGAG AGTTTTAAAA AACAAAACAA TGTAAGTAAA    60
GGATATTTCT GAATCTTAAA ATTCATCCCA TGTGTGATCA TAAACTCATA AAAATAATTT   120
TAAGATGTCG GAAAAGGATA CTTTGATTAA ATAAAAACAC TCATGGATAT GTAAAAACTG   180
TCAAGATTAA AATTTAATAG TTTCATTTAT TTGTTATTTT ATTTGTAAG                229
```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 3043 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
CTAGAGAGGA ACAATGGGGT TATTCAGAGG TTTTGTTTTC CTCTTAGTTC TGTGCCTGCT    60
GCACCAGTCA AATACTTCCT TCATTAAGCT GAATAATAAT GGCTTTGAAG ATATTGTCAT   120
TGTTATAGAT CCTAGTGTGC CAGAAGATGA AAAAATAATT GAACAAATAG AGGATATGGT   180
GACTACAGCT TCTACGTACC TGTTTGAAGC CACAGAAAAA AGATTTTTTT TCAAAAATGT   240
ATCTATATTA ATTCCTGAGA ATTGGAAGGA AAATCCTCAG TACAAAAGGC CAAAACATGA   300
AAACCATAAA CATGCTGATG TTATAGTTGC ACCACCTACA CTCCCAGGTA GAGATGAACC   360
ATACACCAAG CAGTTCACAG AATGTGGAGA GAAAGGCGAA TACATTCACT TCACCCCTGA   420
CCTTCTACTT GAAAAAAAAC AAAATGAATA TGGACCACCA GGCAAACTGT TTGTCCATGA   480
GTGGGCTCAC CTCCGGTGGG GAGTGTTTGA TGAGTACAAT GAAGATCAGC CTTTCTACCG   540
TGCTAAGTCA AAAAAAATCG AAGCAACAAG GTGTTCCGCA GGTATCTCTG GTAGAAATAG   600
AGTTTATAAG TGTCAAGGAG GCAGCTGTCT TAGTAGAGCA TGCAGAATTG ATTCTACAAC   660
AAAACTGTAT GGAAAAGATT GTCAATTCTT TCCTGATAAA GTACAAACAG AAAAAGCATC   720
CATAATGTTT ATGCAAAGTA TTGATTCTGT TGTTGAATTT GTAACGAAA AAACCCATAA    780
TCAAGAAGCT CCAAGCCTAC AAAACATAAA GTGCAATTTT AGAAGTACAT GGGAGGTGAT   840
TAGCAATTCT GAGGATTTTA AAAACACCAT ACCCATGGTG ACACCACCTC CTCCACCTGT   900
```

```
CTTCTCATTG CTGAAGATCA GTCAAAGAAT TGTGTGCTTA GTTCTTGATA AGTCTGGAAG    960
CATGGGGGGT AAGGACCGCC TAAATCGAAT GAATCAAGCA GCAAACATT  TCCTGCTGCA   1020
GACTGTTGAA AATGGATCCT GGGTGGGGAT GGTTCACTTT GATAGTACTG CCACTATTGT   1080
AAATAAGCTA ATCCAAATAA AAAGCAGTGA TGAAAGAAAC ACACTCATGG CAGGATTACC   1140
TACATATCCT CTGGGAGGAA CTTCCATCTG CTCTGGAATT AAATATGCAT TTCAGGTGAT   1200
TGGAGAGCTA CATTCCCAAC TCGATGGATC CGAAGTACTG CTGCTGACTG ATGGGGAGGA   1260
TAACACTGCA AGTTCTTGTA TTGATGAAGT GAAACAAAGT GGGGCCATTG TTCATTTTAT   1320
TGCTTTGGGA AGAGCTGCTG ATGAAGCAGT AATAGAGATG AGCAAGATAA CAGGAGGAAG   1380
TCATTTTTAT GTTTCAGATG AAGCTCAGAA CAATGGCCTC ATTGATGCTT TTGGGGCTCT   1440
TACATCAGGA AATACTGATC TCTCCCAGAA GTCCCTTCAG CTCGAAAGTA AGGGATTAAC   1500
ACTGAATAGT AATGCCTGGA TGAACGACAC TGTCATAATT GATAGTACAG TGGGAAAGGA   1560
CACGTTCTTT CTCATCACAT GGAACAGTCT GCCTCCCAGT ATTTCTCTCT GGGATCCCAG   1620
TGGAACAATA ATGGAAAATT TCACAGTGGA TGCAACTTCC AAAATGGCCT ATCTCAGTAT   1680
TCCAGGAACT GCAAAGGTGG GCACTTGGGC ATACAATCTT CAAGCCAAAG CGAACCCAGA   1740
AACATTAACT ATTACAGTAA CTTCTCGAGC AGCAAATTCT TCTGTGCCTC CAATCACAGT   1800
GAATGCTAAA ATGAATAAGG ACGTAAACAG TTTCCCCAGC CCAATGATTG TTTACGCAGA   1860
AATTCTACAA GGATATGTAC CTGTTCTTGG AGCCAATGTG ACTGCTTTCA TTGAATCACA   1920
GAATGGACAT ACAGAAGTTT TGGAACTTTT GGATAATGGT GCAGGCGCTG ATTCTTTCAA   1980
GAATGATGGA GTCTACTCCA GGTATTTTAC AGCATATACA GAAAATGGCA GATATAGCTT   2040
AAAAGTTCGG GCTCATGGAG GAGCAAACAC TGCCAGGCTA AAATTACGGC CTCCACTGAA   2100
TAGAGCCGCG TACATACCAG GCTGGGTAGT GAACGGGGAA ATTGAAGCAA ACCCGCCAAG   2160
ACCTGAAATT GATGAGGATA CTCAGACCAC CTTGGAGGAT TTCAGCCGAA CAGCATCCGG   2220
AGGTGCATTT GTGGTATCAC AAGTCCCAAG CCTTCCCTTG CCTGACCAAT ACCCACCAAG   2280
TCAAATCACA GACCTTGATG CCACAGTTCA TGAGGATAAG ATTATTCTTA CATGGACAGC   2340
ACCAGGAGAT AATTTTGATG TTGGAAAAGT TCAACGTTAT ATCATAAGAA TAAGTGCAAG   2400
TATTCTTGAT CTAAGAGACA GTTTTGATGA TGCTCTTCAA GTAAATACTA CTGATCTGTC   2460
ACCAAAGGAG GCCAACTCCA AGGAAAGCTT TGCATTTAAA CCAGAAAATA TCTCAGAAGA   2520
AAATGCAACC CACATATTTA TTGCCATTAA AAGTATAGAT AAAAAGCAATT TGACATCAAA   2580
AGTATCCAAC ATTGCACAAG TAACTTTGTT TATCCCTCAA GCAAATCCTG ATGACATTGA   2640
TCCTACTCCT ACTCCTACTC CTACTCCTGA TAAAAGTCAT AATTCTGGAG TTAATATTTC   2700
TACGCTGGTA TTGTCTGTGA TTGGGTCTGT TGTAATTGTT AACTTTATTT TAAGTACCAC   2760
CATTTGAACC TTAACGAAGA AAAAAATCTT CAAGTAGACC TAGAAGAGAG TTTTAAAAAA   2820
CAAAACAATG TAAGTAAAGG ATATTTCTGA ATCTTAAAAT TCATCCCATG TGTGATCATA   2880
AACTCATAAA AATAATTTTA AGATGTCGGA AAAGGATACT TTGATTAAAT AAAAACACTC   2940
ATGGATATGT AAAAACTGTC AAGATTAAAA TTTAATAGTT TCATTTATTT GTTATTTTAT   3000
TTGTAAGAAA TAGTGATGAA CAAAGATCCT TTTTCATACT GAT                     3043
```

(2) INFORMATION FOR SEQ ID NO:17:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 1399 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear


   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
GCAAATTCTT CTGTGCCTCC AATCACAGTG AATGCTAAAA TGAATAAGGA CGTAAACAGT    60
TTCCCCAGCC CAATGATTGT TTACGCAGAA ATTCTACAAG GATATGTACC TGTTCTTGGA   120
GCCAATGTGA CTGCTTTCAT TGAATCACAG AATGGACATA CAGAAGTTTT GGAACTTTTG   180
GATAATGGTG CAGGCGCTGA TTCTTTCAAG AATGATGGAG TCTACTCCAG GTATTTTACA   240
GCATATACAG AAAATGGCAG ATATAGCTTA AAAGTTCGGG CTCATGGAGG AGCAAACACT   300
GCCAGGCTAA AATTACGGCC TCCACTGAAT AGAGCCGCGT ACATACCAGG CTGGGTAGTG   360
AACGGGGAAA TTGAAGCAAA CCCGCCAAGA CCTGAAATTG ATGAGGATAC TCAGACCACC   420
TTGGAGGATT TCAGCCGAAC AGCATCCGGA GGTGCATTTG TGGTATCACA AGTCCCAAGC   480
CTTCCCTTGC CTGACCAATA CCCACCAAGT CAAATCACAG ACCTTGATGT CACAGTTCAT   540
GAGGATAAGA TTATTCTTAC ATGGACAGCA CCAGGAGATA ATTTTGATGT TGGAAAAGTT   600
CAACGTTATA TCATAAGAAT AAGTGCAAGT ATTCTTGATC TAAGAGACAG TTTTGATGAT   660
GCTCTTCAAG TAAATACTAC TGATCTGTCA CCAAAGGAGG CCAACTCCAA GGAAAGCTTT   720
GCATTTAAAC CAGAAAATAT CTCAGAAGAA AATGCAACCC ACATATTTAT TGCCATTAAA   780
AGTATAGATA AAAGCAATTT GACATCAAAA GTATCCAACA TTGCACAAGT AACTTTGTTT   840
ATCCCTCAAG CAAATCCTGA TGACATTGAT CCTACTCCTA CTCCTACTCC TACTCCTGAT   900
AAAAGTCATA ATTCTGGAGT TAATATTTCT ACGCTGGTAT TGTCTGTGAT TGGGTCTGTT   960
GTAATTGTTA ACTTTATTTT AAGTACCACC ATTTGAACCT TAACGAAGAA AAAAATCTTC   1020
```

```
AAGTAGACCT AGAAGAGAGT TTTAAAAAAC AAAACAATGT AAGTAAAGGA TATTTCTGAA    1080
TCTTAAAATT CATCCCATGT GTGATCATAA ACTCATAAAA ATAATTTTAA GATGTCGGAA    1140
AAGGATACTT TGATTAAATA AAAACACTCA TGGATATGTA AAAACTGTCA AGATTAAAAT    1200
TTAATAGTTT CATTTATTTG TTATTTTATT TGTAAGAAAT AGTGATGAAC AAAGATCCTT    1260
TTTCATACTG ATACCTGGTT GTATATTATT TGATGCAACA GTTTTCTGAA ATGATATTTC    1320
AAATTGCATC AAGAAATTAA AATCATCTAT CTGAGTAGTC AAAATACAAG TAAAGGAGAG    1380
CAAATAAACA ACATTTGGA                                                 1399
```

(2) INFORMATION FOR SEQ ID NO:18:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3181 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
GCCAGGAATA ACTAGAGAGG AACAATGGGG TTATTCAGAG GTTTTGTTTT CCTCTTAGTT      60
CTGTGCCTGC TGCACCAGTC AAATACTTCC TTCATTAAGC TGAATAATAA TGGCTTTGAA     120
GATATTGTCA TTGTTATAGA TCCTAGTGTG CCAGAAGATG AAAAAATAAT TGAACAAATA     180
GAGGATATGG TGACTACAGC TTCTACGTAC CTGTTTGAAG CCACAGAAAA AAGATTTTTT     240
TTCAAAAATG TATCTATATT AATTCCTGAG AATTGGAAGG AAAATCCTCA GTACAAAAGG     300
CCAAACATG AAAACCATAA ACATGCTGAT GTTATAGTTG CACCACCTAC ACTCCCAGGT     360
AGAGATGAAC CATACACCAA GCAGTTCACA GAATGTGGAG AGAAAGGCGA ATACATTCAC     420
TTCACCCCTG ACCTTCTACT TGAAAAAAAA CAAAATGAAT ATGGACCACC AGGCAAACTG     480
TTTGTCCATG AGTGGGCTCA CCTCCGGTGG GGAGTGTTTG ATGAGTACAA TGAAGATCAG     540
CCTTTCTACC GTGCTAAGTC AAAAAAAATC GAAGCAACAA GGTGTTCCGC AGGTATCTCT     600
GGTAGAAATA GAGTTTATAA GTGTCAAGGA GGCAGCTGTC TTAGTAGAGC ATGCAGAATT     660
GATTCTACAA CAAAACTGTA TGGAAAAGAT TGTCAATTCT TTCCTGATAA AGTACAAACA     720
GAAAAAGCAT CCATAATGTT TATGCAAAGT ATTGATTCTG TTGTTGAATT TTGTAACGAA     780
AAAACCCATA ATCAAGAAGC TCCAAGCCTA CAAAACATAA AGTGCAATTT TAGAAGTACA     840
TGGGAGGTGA TTAGCAATTC TGAGGATTTT AAAAACACCA TACCCATGGT GACACCACCT     900
CCTCCACCTG TCTTCTCATT GCTGAAGATC AGTCAAAGAA TTGTGTGCTT AGTTCTTGAT     960
AAGTCTGGAA GCATGGGGGG TAAGGACCGC CTAAATCGAA TGAATCAAGC AGCAAAACAT    1020
TTCCTGCTGC AGACTGTTGA AAATGGATCC TGGGTGGGGA TGGTTCACTT TGATAGTACT    1080
GCCACTATTG TAAATAAGCT AATCCAAATA AAAAGCAGTG ATGAAAGAAA CACACTCATG    1140
GCAGGATTAC CTACATATCC TCTGGGAGGA ACTTCCATCT GCTCTGGAAT TAAATATGCA    1200
TTTCAGGTGA TTGGAGAGCT ACATTCCCAA CTCGATGGAT CCGAAGTACT GCTGCTGACT    1260
GATGGGGAGG ATAACACTGC AAGTTCTTGT ATTGATGAAG TGAAACAAAG TGGGGCCATT    1320
GTTCATTTTA TTGCTTTGGG AAGAGCTGAT GATGAAGCAG TAATAGAGAT GAGCAAGATA    1380
ACAGGAGGAA GTCATTTTTA TGTTTCAGAT GAAGCTCAGA ACAATGGCCT CATTGATGCT    1440
TTTGGGGCTC TTACATCAGG AAATACTGAT CTCTCCCAGA AGTCCCTTCA GCTCGAAAGT    1500
AAGGGATTAA CACTGAATAG TAATGCCTGG ATGAACGACA CTGTCATAAT TGATAGTACA    1560
GTGGGAAAGG ACACGTTCTT TCTCATCACA TGGAACAGTC TGCCTCCCAG TATTTCTCTC    1620
TGGGATCCCA GTGGAACAAT AATGGAAAAT TTCACAGTGG ATGCAACTTC CAAAATGGCC    1680
TATCTCAGTA TTCCAGGAAC TGCAAAGGTG GGCACTTGGG CATACAATCT TCAAGCCAAA    1740
GCGAACCCAG AAACATTAAC TATTACAGTA ACTTCTCGAG CAGCAAATTC TTCTGTGCCT    1800
CCAATCACAG TGAATGCTAA AATGAATAAG GACGTAAACA GTTTCCCCAG CCCAATGATT    1860
GTTTACGCAG AAATTCTACA AGGATATGTA CCTGTTCTTG GAGCCAATGT GACTGCTTTC    1920
ATTGAATCAC AGAATGGACA TACAGAAGTT TGGAACTTT TGGATAATGG TGCAGGCGCT    1980
GATTCTTTCA AGAATGATGG AGTCTACTCC AGGTATTTTA CAGCATATAC AGAAAATGGC    2040
AGATATAGCT TAAAAGTTCG GGCTCATGGA GGAGCAAACA CTGCCAGGCT AAAAATTACGG    2100
CCTCCACTGA ATAGAGCCGC GTACATACCA GGCTGGGTAG TGAACGGGGA AATTGAAGCA    2160
AACCCGCCAA GACCTGAAAT TGATGAGGAT ACTCAGACCA CCTTGGAGGA TTTCAGCCGA    2220
ACAGCATCCG GAGGTGCATT TGTGGTATCA CAAGTCCCAA GCCTTCCCTT GCCTGACCAA    2280
TACCCACCAA GTCAAATCAC AGACCTTGAT GCCACAGTTC ATGAGGATAA GATTATTCTT    2340
ACATGGACAG CACCAGGAGA TAATTTTGAT GTTGGAAAAG TTCAACGTTA TATCATAAGA    2400
ATAAGTGCAA GTATTCTTGA TCTAAGAGAC AGTTTTGATG ATGCTCTTCA AGTAAATACT    2460
ACTGATCTGT CACCAAAGGA GGCCAACTCC AAGGAAAGCT TTGCATTTAA ACCAGAAAAT    2520
ATCTCAGAAG AAAATGCAAC CCACATATTT ATTGCCATTA AAGTATGGAA TAAAAGCAAT    2580
TTGACATCAA AAGTATCCAA CATTGCACAA GTAACTTTGT TTATCCCTCA AGCAAATCCT    2640
GATGACATTG ATCCTACTCC TACTCCTACT CCTACTCCTG ATAAAAGTCA TAATTCTGGA    2700
GTTAATATTT CTACGCTGGT ATTGTCTGTG ATTGGGTCTG TTGTAATTGT TAACTTTATT    2760
TTAAGTACCA CCATTTGAAC CTTAACGAAG AAAAAAATCT TCAAGTAGAC CTAGAAGAGA    2820
```

```
GTTTTAAAAA ACAAAACAAT GTAAGTAAAG GATATTTCTG AATCTTAAAA TTCATCCCAT      2880
GTGTGATCAT AAACTCATAA AAATAATTTT AAGATGTCGG AAAAGGATAC TTTGATTAAA      2940
TAAAAACACT CATGGATATG TAAAAACTGT CAAGATTAAA ATTTAATAGT TTCATTTATT      3000
TGTTATTTTA TTTGTAAGAA ATAGTGATGA ACAAAGATCC TTTTTCATAC TGATACCTGG      3060
TTGTATATTA TTTGATGCAA CAGTTTTCTG AAATGATATT TCAAATTGCA TCAAGAAATT      3120
AAAATCATCT ATCTGAGTAG TCAAAATACA AGTAAAGGAG AGCAAATAAA CAACATTTGG      3180
A                                                                      3181
```

          (2) INFORMATION FOR SEQ ID NO:19:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 68 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear


     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
AGCTCGGAAT TCCGAGCTTG GATCCTCTAG AGCGGCCGCC GACTAGTGAG CTCGTCGACC      60
CGGGAATT                                                               68
```

          (2) INFORMATION FOR SEQ ID NO:20:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 68 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear


     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
AATTAATTCC CGGGTCGACG AGCTCACTAG TCGGCGGCCG CTCTAGAGGA TCCAAGCTCG      60
GAATTCCG                                                               68
```

          (2) INFORMATION FOR SEQ ID NO:21:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear


     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```
AGCGGATAAC AATTTCACAC AGGA                                             24
```

          (2) INFORMATION FOR SEQ ID NO:22:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear


     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```
TGTAAAACGA CGGCCAGT                                                    18
```

          (2) INFORMATION FOR SEQ ID NO:23:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs

```
            (B)  TYPE:  nucleic acid
            (C)  STRANDEDNESS:  single
            (D)  TOPOLOGY:  linear


      (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:23:

CTGCCAGGCT AAAATTACGG                                             20

            (2)  INFORMATION FOR SEQ ID NO:24:

      (i)  SEQUENCE CHARACTERISTICS:
            (A)  LENGTH:  20 base pairs
            (B)  TYPE:  nucleic acid
            (C)  STRANDEDNESS:  single
            (D)  TOPOLOGY:  linear


      (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:24:

ATCACAGACC TTGATGCCAC                                             20

            (2)  INFORMATION FOR SEQ ID NO:25:

      (i)  SEQUENCE CHARACTERISTICS:
            (A)  LENGTH:  24 base pairs
            (B)  TYPE:  nucleic acid
            (C)  STRANDEDNESS:  single
            (D)  TOPOLOGY:  linear


      (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:25:

GCTGGTATTG TCTGTGATTG GGTC                                        24

            (2)  INFORMATION FOR SEQ ID NO:26:

      (i)  SEQUENCE CHARACTERISTICS:
            (A)  LENGTH:  20 base pairs
            (B)  TYPE:  nucleic acid
            (C)  STRANDEDNESS:  single
            (D)  TOPOLOGY:  linear


      (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:26:

CATCAGGATT TGCTTGAGGG                                             20

            (2)  INFORMATION FOR SEQ ID NO:27:

      (i)  SEQUENCE CHARACTERISTICS:
            (A)  LENGTH:  20 base pairs
            (B)  TYPE:  nucleic acid
            (C)  STRANDEDNESS:  single
            (D)  TOPOLOGY:  linear


      (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:27:

TATTGGTCAG GCAAGGGAAG                                             20

            (2)  INFORMATION FOR SEQ ID NO:28:

      (i)  SEQUENCE CHARACTERISTICS:
            (A)  LENGTH:  20 base pairs
            (B)  TYPE:  nucleic acid
```

```
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear


           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTGTTTGCTC CTCCATGAGC                                        20


              (2) INFORMATION FOR SEQ ID NO:29:

           (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 20 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear


           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAAGTAGAAG GTCAGGGGTG                                        20


              (2) INFORMATION FOR SEQ ID NO:30:

           (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 20 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear


           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATAAGTGTCA AGGAGGCAGC                                        20


              (2) INFORMATION FOR SEQ ID NO:31:

           (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 20 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear


           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCAGACTGTT CCATGTGATG                                        20


              (2) INFORMATION FOR SEQ ID NO:32:

           (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 20 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: single
                    (D) TOPOLOGY: linear


           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATGTACCTGT TCTTGGAGCC                                        20


              (2) INFORMATION FOR SEQ ID NO:33:

           (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 20 base pairs
                    (B) TYPE: nucleic acid
```

```
    (C)  STRANDEDNESS: single
    (D)  TOPOLOGY: linear


    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:33:

ACGTACCTGT TTGAAGCCAC                                        20

        (2)  INFORMATION FOR SEQ ID NO:34:

    (i)  SEQUENCE CHARACTERISTICS:
      (A)  LENGTH: 20 base pairs
      (B)  TYPE: nucleic acid
      (C)  STRANDEDNESS: single
      (D)  TOPOLOGY: linear


    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGTAAGGACC GCCTAAATCG                                        20

        (2)  INFORMATION FOR SEQ ID NO:35:

    (i)  SEQUENCE CHARACTERISTICS:
      (A)  LENGTH: 20 base pairs
      (B)  TYPE: nucleic acid
      (C)  STRANDEDNESS: single
      (D)  TOPOLOGY: linear


    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:35:

GAAGTGAAAC AAAGTGGGGC                                        20

        (2)  INFORMATION FOR SEQ ID NO:36:

    (i)  SEQUENCE CHARACTERISTICS:
      (A)  LENGTH: 20 base pairs
      (B)  TYPE: nucleic acid
      (C)  STRANDEDNESS: single
      (D)  TOPOLOGY: linear


    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTATCCTCCC CATCAGTCAG                                        20

        (2)  INFORMATION FOR SEQ ID NO:37:

    (i)  SEQUENCE CHARACTERISTICS:
      (A)  LENGTH: 20 base pairs
      (B)  TYPE: nucleic acid
      (C)  STRANDEDNESS: single
      (D)  TOPOLOGY: linear


    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:37:

TCGATTTAGG CGGTCCTTAC                                        20

        (2)  INFORMATION FOR SEQ ID NO:38:

    (i)  SEQUENCE CHARACTERISTICS:
      (A)  LENGTH: 20 base pairs
      (B)  TYPE: nucleic acid
      (C)  STRANDEDNESS: single
```

(D) TOPOLOGY: linear


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TGTGGCTTCA AACAGGTACG                                                    20

        (2) INFORMATION FOR SEQ ID NO:39:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 25 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear


        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GGGTAAGGAC CGCCTAAATC GAATG                                              25

        (2) INFORMATION FOR SEQ ID NO:40:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 23 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear


        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GAGCCCCAAA AGCATCAATG AGG                                                23


        (2) INFORMATION FOR SEQ ID NO:41:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 917 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: None

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Met Gly Leu Phe Arg Gly Phe Val Phe Leu Leu Val Leu Cys Leu Leu
1               5                   10                  15
His Gln Ser Asn Thr Ser Phe Ile Lys Leu Asn Asn Asn Gly Phe Glu
            20                  25                  30
Asp Ile Val Ile Val Ile Asp Pro Ser Val Pro Glu Asp Glu Lys Ile
            35                  40                  45
Ile Glu Gln Ile Glu Asp Met Val Thr Thr Ala Ser Thr Tyr Leu Phe
        50                  55                  60
Glu Ala Thr Glu Lys Arg Phe Phe Phe Lys Asn Val Ser Ile Leu Ile
65                  70                  75                  80
Pro Glu Asn Trp Lys Glu Asn Pro Gln Tyr Lys Arg Pro Lys His Glu
                85                  90                  95
Asn His Lys His Ala Asp Val Ile Val Ala Pro Pro Thr Leu Pro Gly
        `   100                 105                 110
Arg Asp Glu Pro Tyr Thr Lys Gln Phe Thr Glu Cys Gly Glu Lys Gly
        115                 120                 125
Glu Tyr Ile His Phe Thr Pro Asp Leu Leu Leu Glu Lys Lys Gln Asn
        130                 135                 140
Glu Tyr Gly Pro Pro Gly Lys Leu Phe Val His Glu Trp Ala His Leu
145                 150                 155                 160

```
Arg Trp Gly Val Phe Asp Glu Tyr Asn Glu Asp Gln Pro Phe Tyr Arg
                165             170             175
Ala Lys Ser Lys Lys Ile Glu Ala Thr Arg Cys Ser Ala Gly Ile Ser
            180             185             190
Gly Arg Asn Arg Val Tyr Lys Cys Gln Gly Gly Ser Cys Leu Ser Arg
        195             200             205
Ala Cys Arg Ile Asp Ser Thr Thr Lys Leu Tyr Gly Lys Asp Cys Gln
    210             215             220
Phe Phe Pro Asp Lys Val Gln Thr Glu Lys Ala Ser Ile Met Phe Met
225             230             235             240
Gln Ser Ile Asp Ser Val Val Glu Phe Cys Asn Glu Lys Thr His Asn
                245             250             255
Gln Glu Ala Pro Ser Leu Gln Asn Ile Lys Cys Asn Phe Arg Ser Thr
            260             265             270
Trp Glu Val Ile Ser Asn Ser Glu Asp Phe Lys Asn Thr Ile Pro Met
        275             280             285
Val Thr Pro Pro Pro Pro Val Phe Ser Leu Leu Lys Ile Ser Gln
        290             295             300
Arg Ile Val Cys Leu Val Leu Asp Lys Ser Gly Ser Met Gly Gly Lys
305             310             315             320
Asp Arg Leu Asn Arg Met Asn Gln Ala Ala Lys His Phe Leu Leu Gln
            325             330             335
Thr Val Glu Asn Gly Ser Trp Val Gly Met Val His Phe Asp Ser Thr
            340             345             350
Ala Thr Ile Val Asn Lys Leu Ile Gln Ile Lys Ser Ser Asp Glu Arg
        355             360             365
Asn Thr Leu Met Ala Gly Leu Pro Thr Tyr Pro Leu Gly Gly Thr Ser
    370             375             380
Ile Cys Ser Gly Ile Lys Tyr Ala Phe Gln Val Ile Gly Glu Leu His
385             390             395             400
Ser Gln Leu Asp Gly Ser Glu Val Leu Leu Leu Thr Asp Gly Glu Asp
            405             410             415
Asn Thr Ala Ser Ser Cys Ile Asp Glu Val Lys Gln Ser Gly Ala Ile
            420             425             430
Val His Phe Ile Ala Leu Gly Arg Ala Ala Asp Glu Ala Val Ile Glu
        435             440             445
Met Ser Lys Ile Thr Gly Gly Ser His Phe Tyr Val Ser Asp Glu Ala
    450             455             460
Gln Asn Asn Gly Leu Ile Asp Ala Phe Gly Ala Leu Thr Ser Gly Asn
465             470             475             480
Thr Asp Leu Ser Gln Lys Ser Leu Gln Leu Glu Ser Lys Gly Leu Thr
            485             490             495
Leu Asn Ser Asn Ala Trp Met Asn Asp Thr Val Ile Ile Asp Ser Thr
            500             505             510
Val Gly Lys Asp Thr Phe Phe Leu Ile Thr Trp Asn Ser Leu Pro Pro
        515             520             525
Ser Ile Ser Leu Trp Asp Pro Ser Gly Thr Ile Met Glu Asn Phe Thr
        530             535             540
Val Asp Ala Thr Ser Lys Met Ala Tyr Leu Ser Ile Pro Gly Thr Ala
545             550             555             560
Lys Val Gly Thr Trp Ala Tyr Asn Leu Gln Ala Lys Ala Asn Pro Glu
            565             570             575
Thr Leu Thr Ile Thr Val Thr Ser Arg Ala Ala Asn Ser Ser Val Pro
            580             585             590
Pro Ile Thr Val Asn Ala Lys Met Asn Lys Asp Val Asn Ser Phe Pro
        595             600             605
Ser Pro Met Ile Val Tyr Ala Glu Ile Leu Gln Gly Tyr Val Pro Val
    610             615             620
Leu Gly Ala Asn Val Thr Ala Phe Ile Glu Ser Gln Asn Gly His Thr
625     ·           630             635             640
Glu Val Leu Glu Leu Leu Asp Asn Gly Ala Gly Ala Asp Ser Phe Lys
            645             650             655
Asn Asp Gly Val Tyr Ser Arg Tyr Phe Thr Ala Tyr Thr Glu Asn Gly
        660             665             670
Arg Tyr Ser Leu Lys Val Arg Ala His Gly Gly Ala Asn Thr Ala Arg
        675             680             685
```

```
Leu Lys Leu Arg Pro Pro Leu Asn Arg Ala Ala Tyr Ile Pro Gly Trp
    690             695                 700
Val Val Asn Gly Glu Ile Glu Ala Asn Pro Pro Arg Pro Glu Ile Asp
705             710             715                         720
Glu Asp Thr Gln Thr Thr Leu Glu Asp Phe Ser Arg Thr Ala Ser Gly
            725             730                     735
Gly Ala Phe Val Val Ser Gln Val Pro Ser Leu Pro Leu Pro Asp Gln
            740             745                 750
Tyr Pro Pro Ser Gln Ile Thr Asp Leu Asp Ala Thr Val His Glu Asp
        755             760             765
Lys Ile Ile Leu Thr Trp Thr Ala Pro Gly Asp Asn Phe Asp Val Gly
    770             775                 780
Lys Val Gln Arg Tyr Ile Ile Arg Ile Ser Ala Ser Ile Leu Asp Leu
785             790             795                         800
Arg Asp Ser Phe Asp Asp Ala Leu Gln Val Asn Thr Thr Asp Leu Ser
            805             810             815
Pro Lys Glu Ala Asn Ser Lys Glu Ser Phe Ala Phe Lys Pro Glu Asn
        820             825             830
Ile Ser Glu Glu Asn Ala Thr His Ile Phe Ile Ala Ile Lys Ser Ile
        835             840             845
Asp Lys Ser Asn Leu Thr Ser Lys Val Ser Asn Ile Ala Gln Val Thr
    850             855             860
Leu Phe Ile Pro Gln Ala Asn Pro Asp Asp Ile Asp Pro Thr Pro Thr
865             870             875                         880
Pro Thr Pro Thr Pro Asp Lys Ser His Asn Ser Gly Val Asn Ile Ser
            885             890                     895
Thr Leu Val Leu Ser Val Ile Gly Ser Val Val Ile Val Asn Phe Ile
            900             905             910
Leu Ser Thr Thr Ile
    915
```

        (2) INFORMATION FOR SEQ ID NO:42:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 21 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: None

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```
Ala Asn Ser Ser Val Pro Pro Ile Thr Val Asn Ala Lys Met Asn Lys
1               5                   10                  15
Asp Val Asn Ser Phe
                20
```

        (2) INFORMATION FOR SEQ ID NO:43:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 31 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear            -

        (ii) MOLECULE TYPE: None

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```
Asp Asn Gly Ala Gly Ala Asp Ser Phe Lys Asn Asp Gly Val Tyr Ser
1               5                   10                  15
Arg Tyr Phe Thr Ala Tyr Thr Glu Asn Gly Arg Tyr Ser Leu Lys
            20                  25                  30
```

        (2) INFORMATION FOR SEQ ID NO:44:

-98-

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 24 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: None

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Val Arg Ala His Gly Gly Ala Asn Thr Ala Arg Leu Lys Leu Arg Pro
1               5                   10                  15
Pro Leu Asn Arg Ala Ala Tyr Ile
            20


        (2) INFORMATION FOR SEQ ID NO:45:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 40 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: None

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ser Leu Pro Leu Pro Asp Gln Tyr Pro Pro Ser Gln Ile Thr Asp Leu
1               5                   10                  15
Asp Ala Thr Val His Glu Asp Lys Ile Ile Leu Thr Trp Thr Ala Pro
            20                  25                  30
Gly Asp Asn Phe Asp Val Gly Lys
            35                  40


        (2) INFORMATION FOR SEQ ID NO:46:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: None

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Tyr Asn Glu Asp Gln Pro Phe Tyr Arg Ala Lys Ser Lys Lys Ile Glu
1               5                   10                  15
Ala Thr Arg Cys
            20

        (2) INFORMATION FOR SEQ ID NO:47:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 24 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: None

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Leu Ser Arg Ala Cys Arg Ile Asp Ser Thr Thr Lys Leu Tyr Gly Lys
1                5                    10              15
Asp Cys Gln Phe Phe Pro Asp Lys
            20

(2) INFORMATION FOR SEQ ID NO:48:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Lys Ser Ser Asp Glu Arg Asn Thr Leu Met Ala Gly Leu Pro Thr Tyr
1                5                    10              15
Pro Leu Gly Gly
            20

(2) INFORMATION FOR SEQ ID NO:49:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 15 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Glu Ile Asp Glu Asp Thr Gln Thr Thr Leu Glu Asp Phe Ser Arg
1                5                    10              15

(2) INFORMATION FOR SEQ ID NO:50:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 8 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Asp Tyr Lys Asp Asp Asp Asp Lys
1                5

(2) INFORMATION FOR SEQ ID NO:51:

    (i) SEQUENCE CHARACTERISTICS:          -
        (A) LENGTH: 21 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Met His Thr Glu His
 1               5                   10          Met His Thr Glu His
                                                             15
His His His His His
                20